

Using 3D Shape Matching in AI DD to Design CCR4 Antagonists

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Please note: this presentation, including questions from the audience, is being recorded and may be made available.

3D Shape Matching in AIDD to Design CCR4 Antagonists

- 3D virtual screening in ADMET Predictor X.5
- AI-driven Drug Design (AIDD) workflow
- CC-chemokine receptor 4 (CCR4) background
- CCR4 receptor antagonists
- Using shape matching in AIDD generate potential CCR4 antagonist

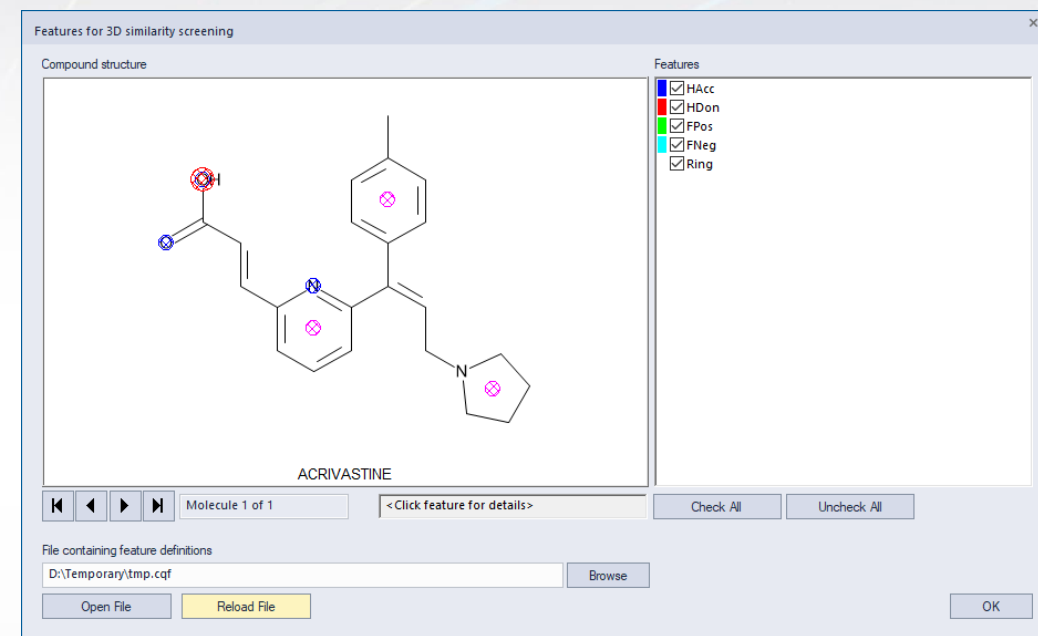
Upcoming features in APX.5

3D Virtual Screening

- Create a 3D conformer database from a set of internally or commercially available compounds
- Perform a similarity screen of the database using one or more reference structures (3D geometry from X-ray or model)
- Similarity screen can run on an NVIDIA GPU for increased performance

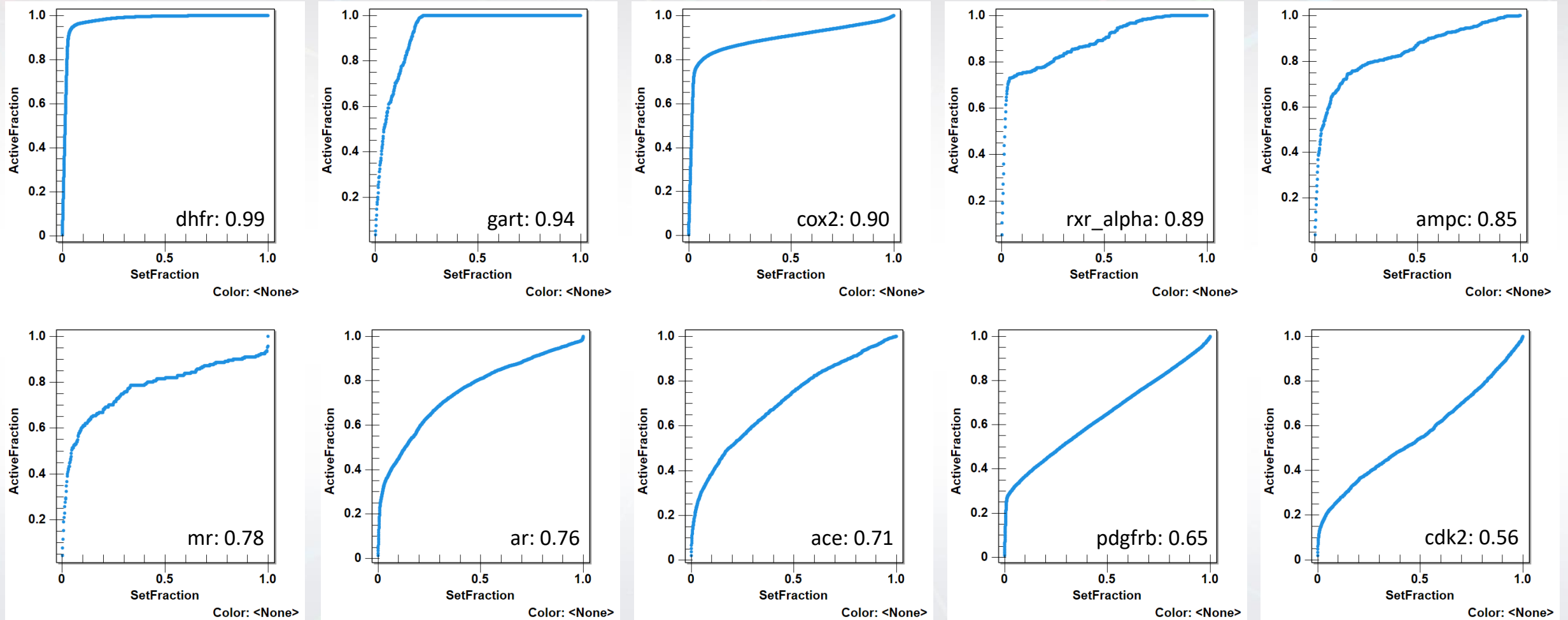
3D Similarity Scores

- Similarity scores consist of a shape term based on overlap volume and a feature term based on the alignment of pharmacophore features; users can adjust the relative importance of the two terms
- Overlap volumes are computed using atom-centered gaussian functions; these allow fast computation and are convenient for gradient based optimization
- Features can include hydrogen bond donors and acceptors, positive and negative charges and ring centroids; users can also define their own features



Features can be defined and visualized using a 2D utility

Performance on the DUD set



Feature weight = 10

Average AUC = 0.78 (40 targets)

AIDD Workflow

Knowledge base

- Protein structure(s)
- Ligand 2D or 3D structures
- SAR
- QSAR models

Optimization

- Pareto selection

Iterate

SEED Molecule(s)

Generate Candidates

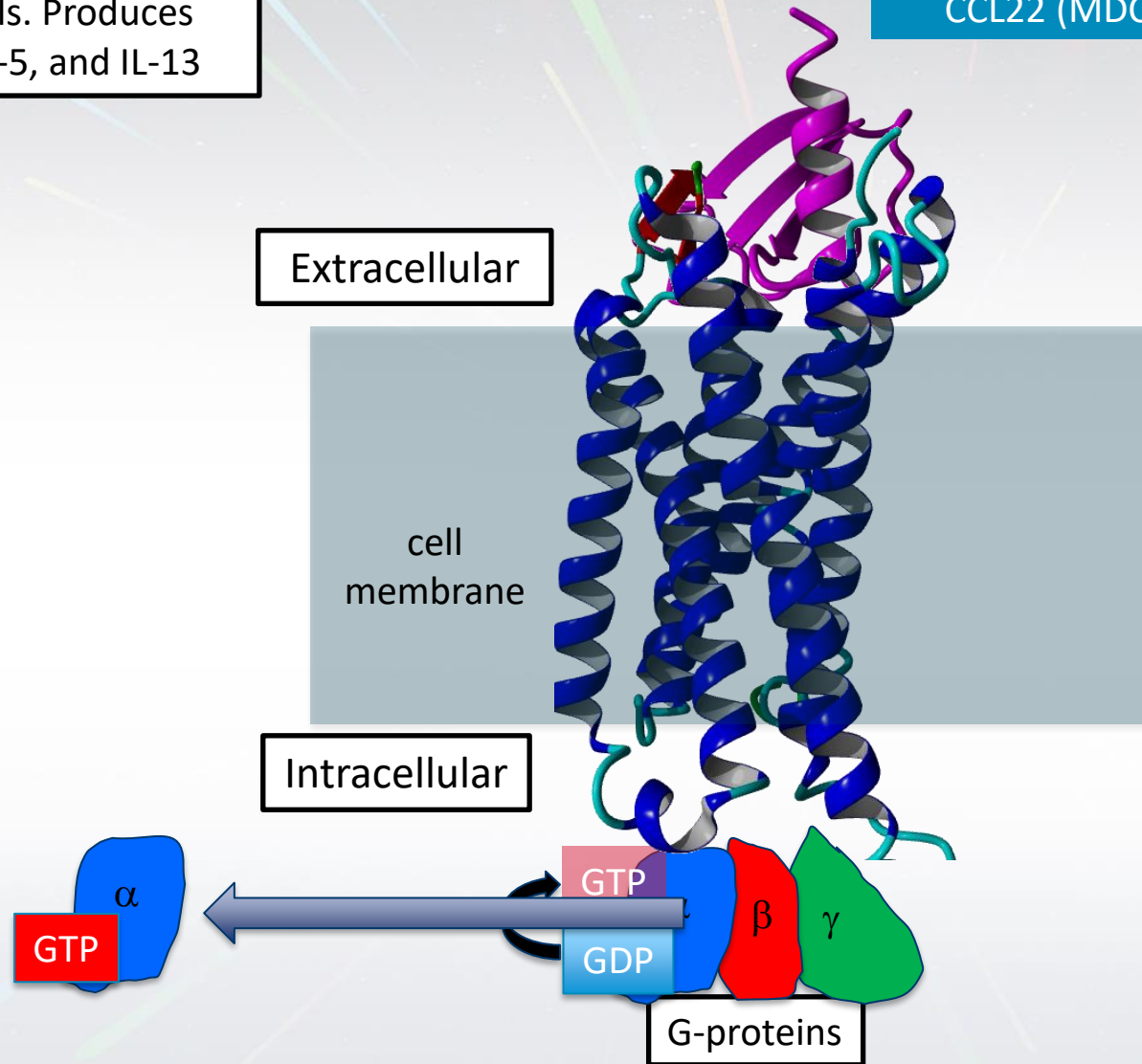
Score

- Predicted target activity
- External programs, e.g., docking
- Synthetic feasibility
- ADMET properties
- Pharmacokinetic properties
- **3D shape matching**

- Apply SMIRKS transformations to randomly-selected compounds from the current population
- SAR - Required substructure
- Remove non-druglike
 - Acetals, Michael acceptors
 - Simple properties, e.g., ≤ 4 aromatic rings

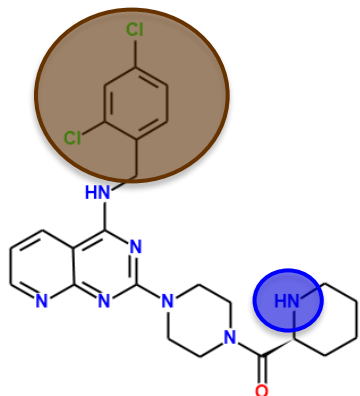
CCR4 is mostly expressed in T helper 2 (Th2) cells. Produces interleukin IL-4, IL-5, and IL-13

CCL17 (TARC) or
CCL22 (MDC)



Small molecule CCR4 antagonists have two distinct allosteric binding sites (Slack et al. 2013) and one site is intracellular (Andrews et al. 2008).

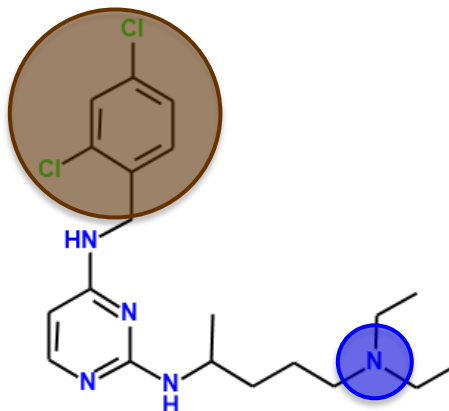
CCR4 S1 Allosteric Antagonists



CHEMBL233046

BMS

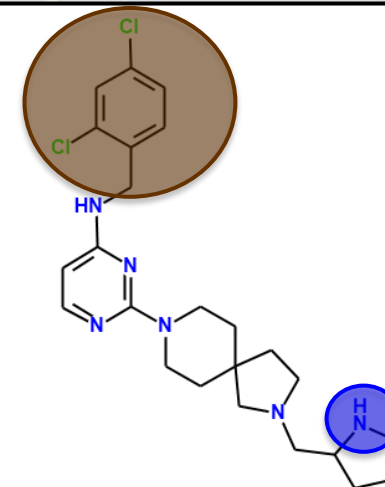
CCR4 FMAT $IC_{50} = 16$ nM
(Purandare et al. 2007)



CHEMBL195298

BMS

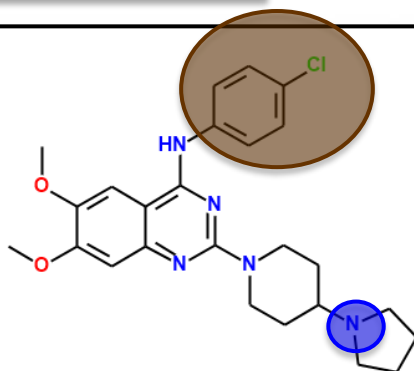
CCR4 $IC_{50} = 270$ nM
(Purandare et al. 2005)



CHEMBL3799266

GSK

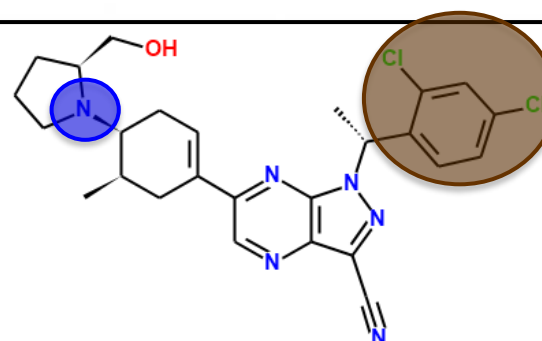
CCR4 TARC disp $IC_{50} = 1.6$ nM
(Shukla et al. 2016)



CHEMBL486840

Astellas

CCR4 GTPgS $IC_{50} = 24$ nM
(Yokoyama et al. 2008)

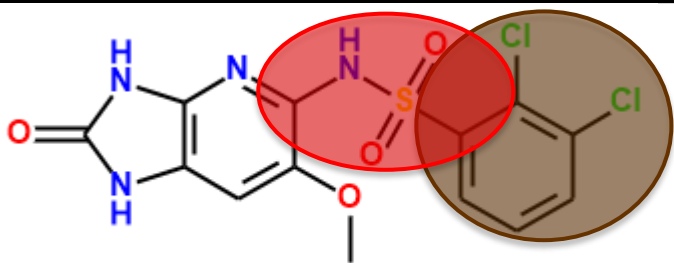


CHEMBL4459231

RAPT Therapeutics

CCR4 Ca flux $IC_{50} = 40$ nM
(Jackson et al. 2019)

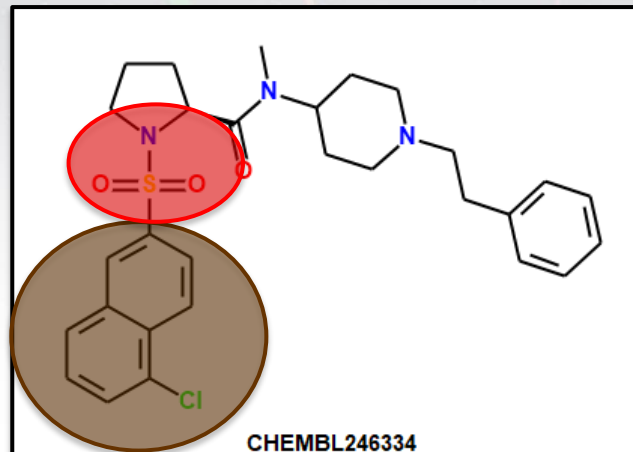
CCR4 S2 Allosteric Antagonists



CHEMBL3310839

GSK

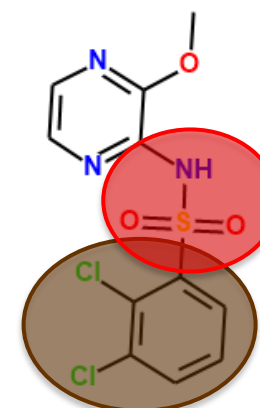
CCR4 GTPgS IC_{50} = 25.1 nM
(Miah et al. 2014)



CHEMBL246334

Millennium

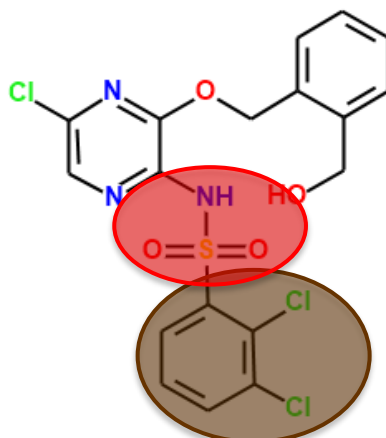
CCR4 MDC disp K_i = 100 nM
(Burdi et al. 2007)



CHEMBL4169247

AstraZeneca

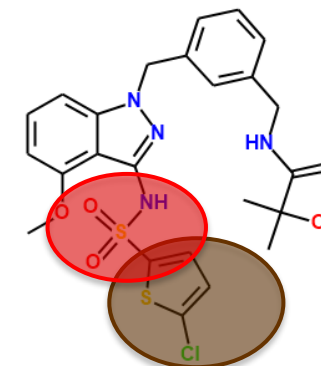
CCR4 FMAT IC_{50} = 15.8 nM
(Kindon et al. 2017)



CHEMBL4172769

AstraZeneca

CCR4 FMAT IC_{50} = 0.316 nM
(Kindon et al. 2017)

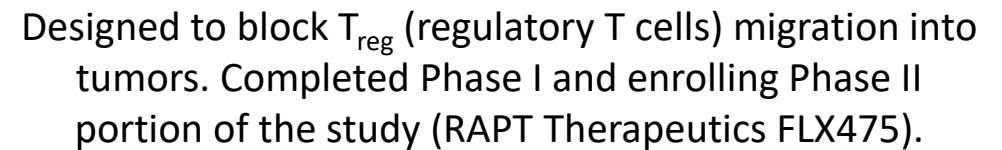
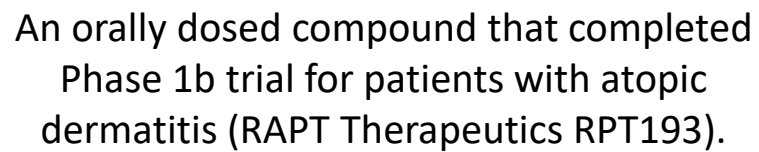


CHEMBL2018969

GSK

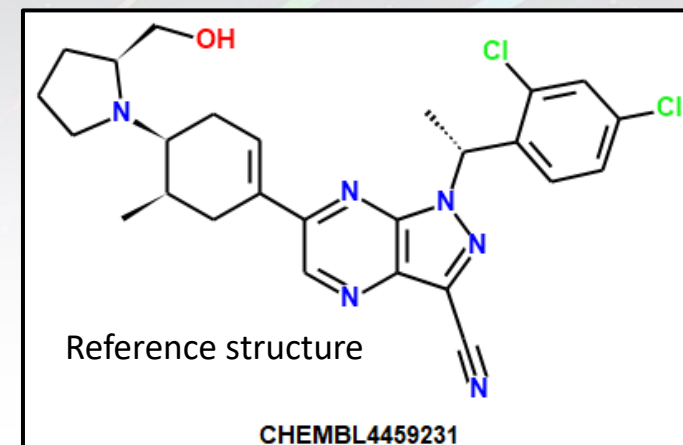
CCR4 GTPgS IC_{50} = 14.8 nM
(Procopiou et al. 2013)

S+ SimulationsPlus
MIDD
Model Informed Drug Development + 2023

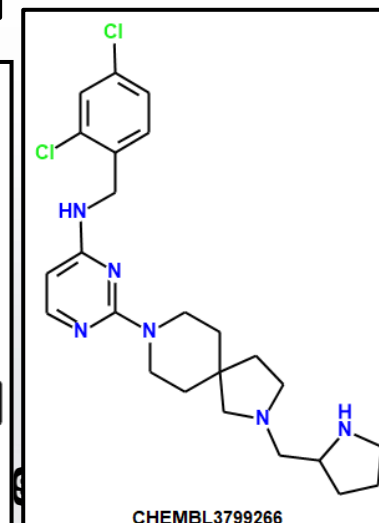
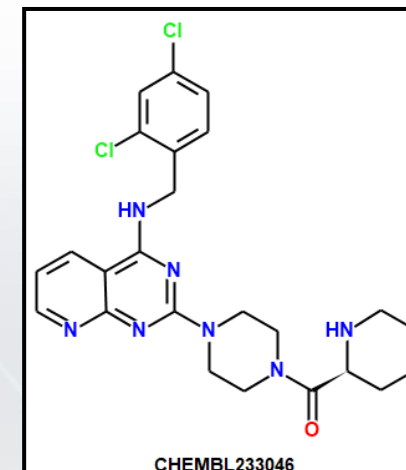
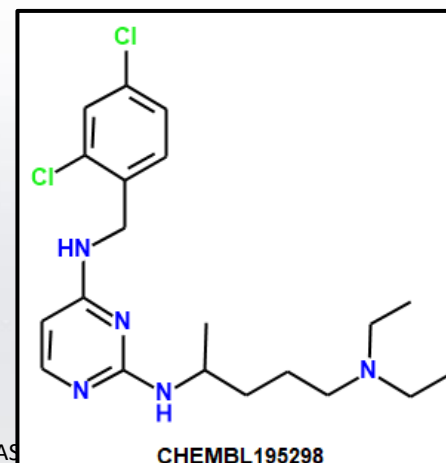
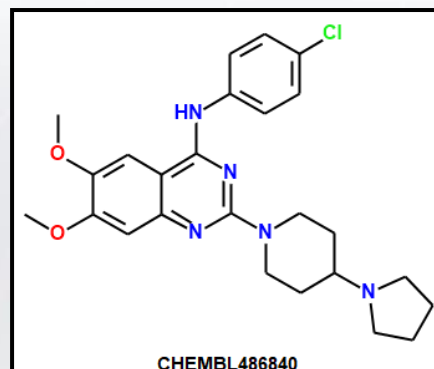


Overlay of Known CCR4 Site 1 Antagonists

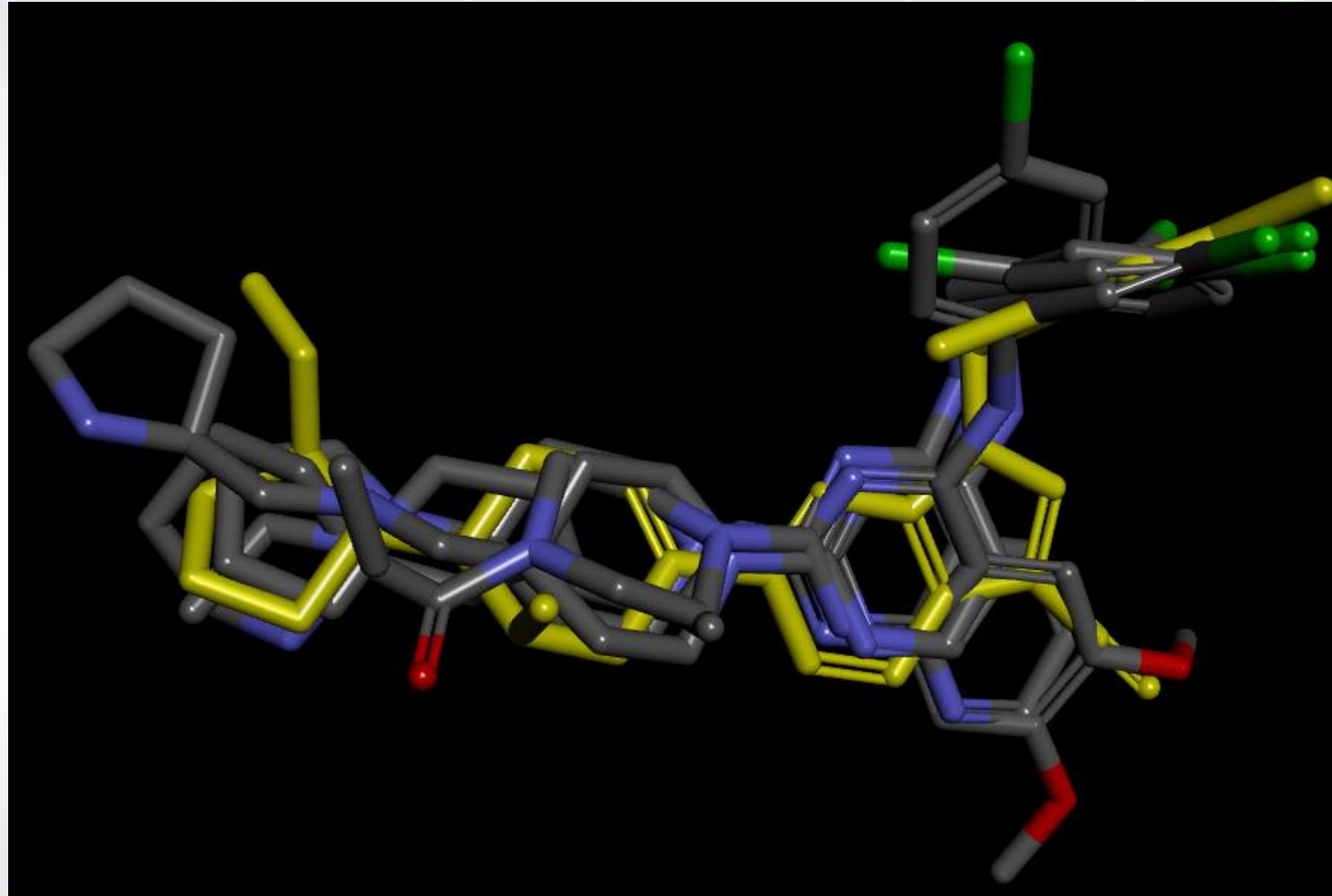
- CHEMBL4459231 reference structure geometry
 - Generate 100 conformations
 - 0.25 minimum RMSD between conformer pairs
 - 10 kcal/mol maximum energy range
 - Minimize lowest energy structure to generate reference geometry
- Candidate database
 - Same as above but store all 101 conformers in database



Candidate database compounds



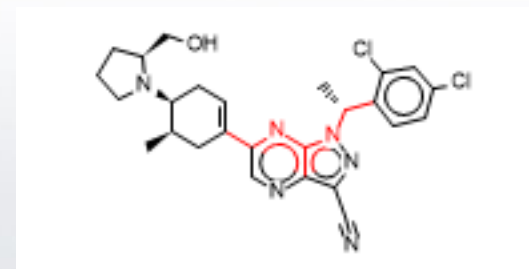
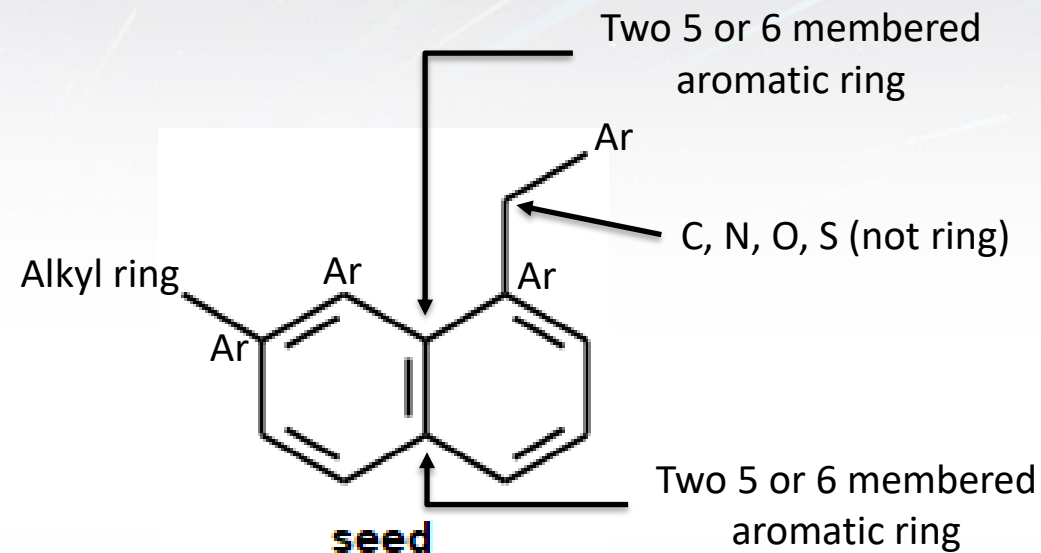
3D Overlay onto RAPT Compound



RAPT compound is colored yellow

AIDD shape matches to RAPT pyrazolopyrazine CCR4 antagonists

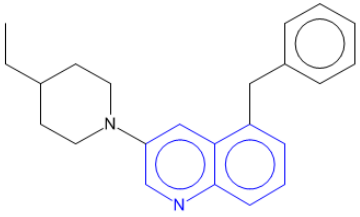
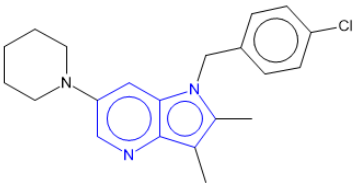
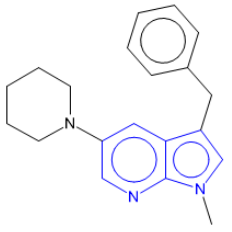
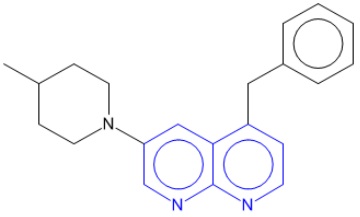
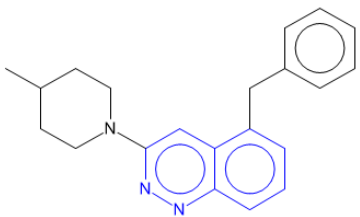
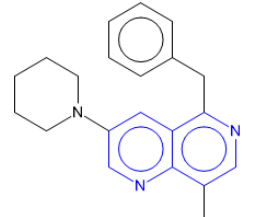
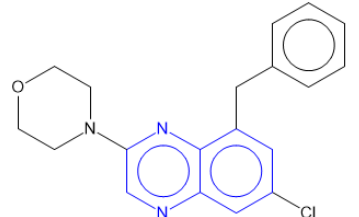
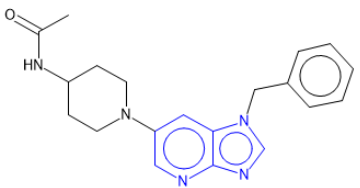
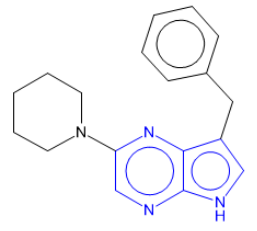
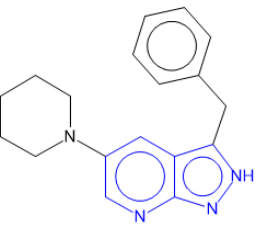
- Use “simple” seed molecule, 1, 7 disubstituted naphthalene
- Objectives
 - Synthetic difficulty
 - Fraction absorbed
 - Tanimoto from shape matching algorithm
- Scaffold query
 - RAFT molecule pharmacophore
([a;r5,r6]([C,O,N,S;!R][a]))[a;r5,r6;R2]([a;r5,r6;R2])[a][a]!@[A;R])
- Druglike filter
 - Limit to 3 Cl, Br, or I (SLQ [Cl,Br,I].[Cl,Br,I].[Cl,Br,I] > 1)
 - Limit to 3 aromatic rings (NPQ ArRing > 3)
 - Limit to 3 CL atoms (SLQ Cl >= 4)
 - Can't match RAPT molecule
- 10 generations
- 500 candidates per generation
- 1000 initial population



Takes about 15 minutes on a DELL laptop
with an Intel(R) Core(TM) i7-10510U CPU @
1.80GHz with an NVIDIA GPU

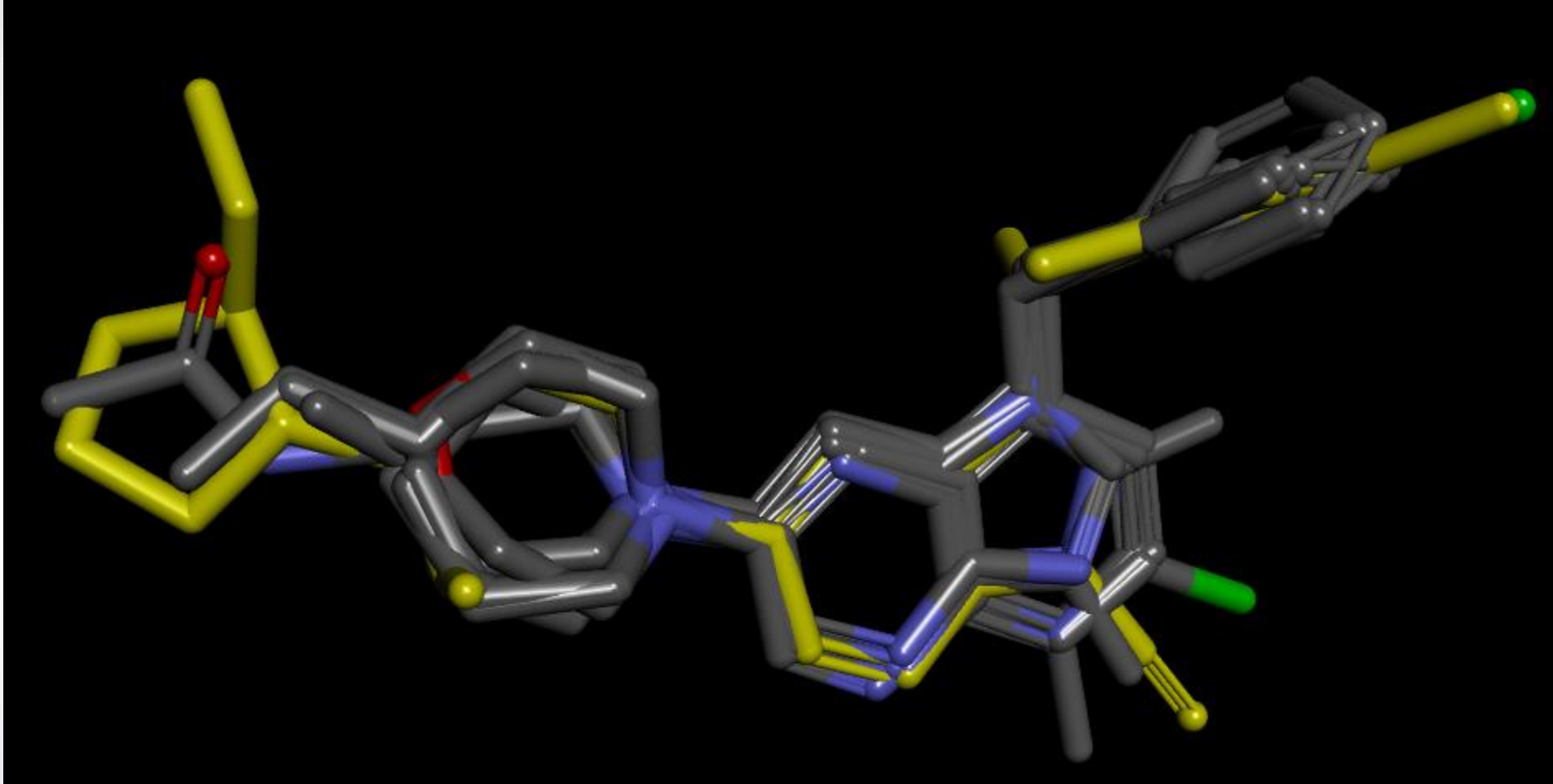
AIDD Results

108 molecules produced, all on the Pareto front

C 1 	C 6 	C 7 	C 2 
C 5 	C 4 	C 3 	C 10 
C 9 	C 8 		

10 scaffolds, highlighted in blue, were produced

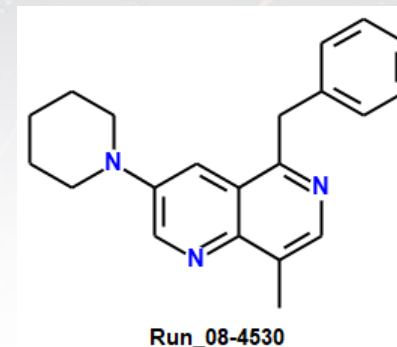
Overlay of AI DD Results on Reference



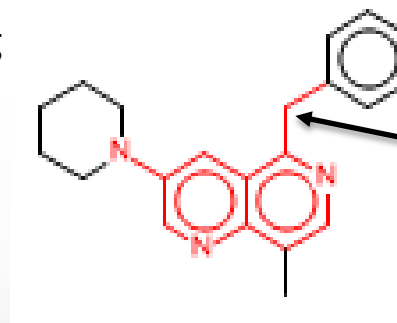
RAPT compound is colored yellow

2nd Round of AIDD

- Use molecule from first run as seed molecule
- 1,6-naphthyridine scaffold
- Objectives
 - Synthetic difficulty
 - Fraction absorbed
 - Tanimoto from shape matching algorithm
- Scaffold query
 - c1([C,O,N,S;!R])[a]n[cH]cc2n[cH]c(!@[A;R])[cH]c21
- Druglike filter
 - Limit to 3 Cl, Br, or I (SLQ [Cl,Br,I].[Cl,Br,I].[Cl,Br,I] > 1)
 - Limit to 3 aromatic rings (NPQ ArRing > 3)
 - Limit to 3 CL atoms (SLQ Cl >= 4)
 - Can't match RAPT molecule
- 10 generations
- 500 candidates per generation
- 1000 initial population



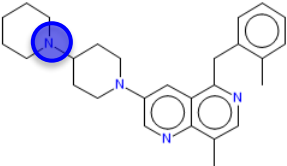
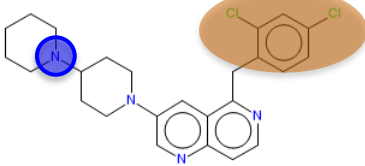
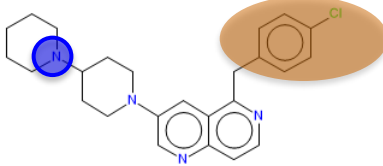
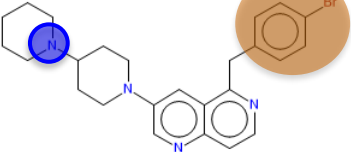
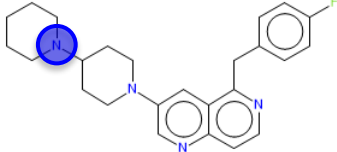
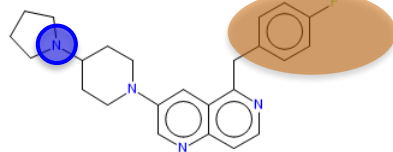
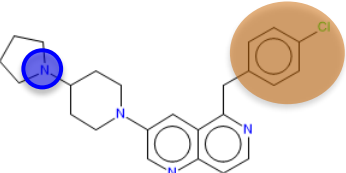
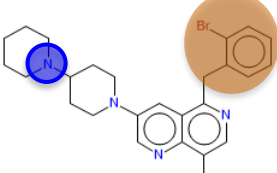
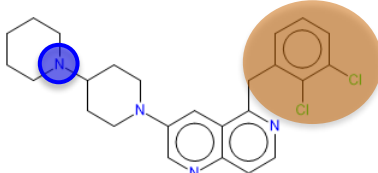
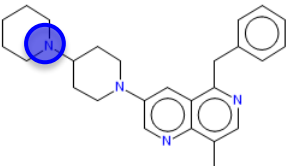
Alkyl ring

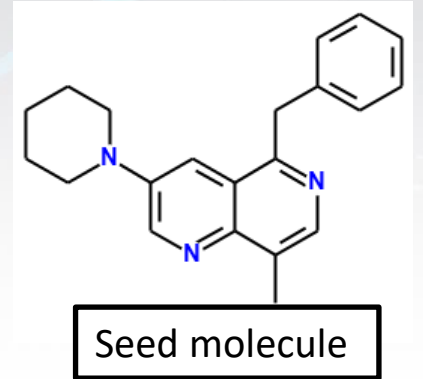


C, N, O, S (not ring)

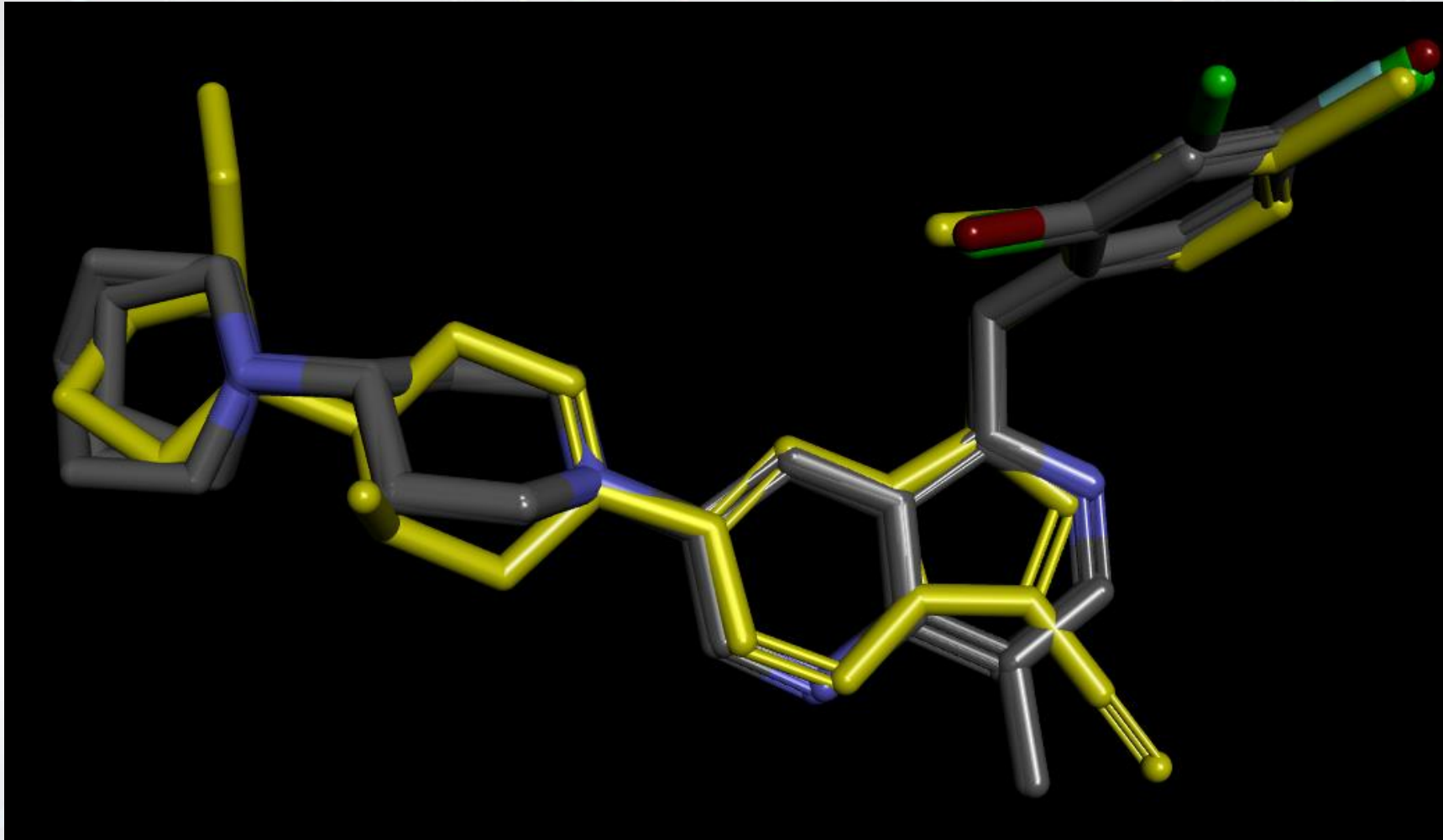
Match from scaffold query

2nd AIDD Run of One Scaffold

2952	0.732	5262	0.730	2987	0.730
					
2956	0.730	3984	0.729	3735	0.729
					
3769	0.728	3615	0.728	4255	0.727
					
1732	0.726	10 best scoring ligands			
					



2nd AIDD Run of One Scaffold



RAPT compound is colored yellow

References

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Miah AH, Abas H, Begg M, Marsh BJ, O'Flynn DE, Ford AJ, Percy JM, Procopiou PA, Richards SA, Rumley SA. (2014) Lead identification of benzimidazolone and azabenzimidazolone arylsulfonamides as CC-chemokine receptor 4 (CCR4) antagonists. *Bioorg. Med. Chem.* 22, 4298-4311.

RAPT Therapeutics RPT193 <https://rapt.com/pipeline/rpt193/>.

RAPT Therapeutics FLX475 <https://rapt.com/pipeline/flx475/>.

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Thanks for watching!

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